(B) sequencing said fragment of DNA to thereby determine the nucleotide sequence of a segment of said fragment, said segment being of a length sufficient to define the nucleotide sequence of a pair of oligonucleotide primers capable of mediating the specific amplification of said fragment;

(C) using said oligonucleotide primers to mediate the specific amplification of DNA obtained from a plurality of other organisms of the same species as said reference organism; and

(D) determining the nucleotide sequences of said amplified DNA molecules of [step C] step (C), and comparing the sequence of said amplified molecules with the sequence of said fragment of said reference organism to thereby identify a single nucleotide polymorphic site.

Please amend Claim 31 as follows:

-- 31 [Amended]. A method for interrogating a polymorphic region of a human single nucleotide polymorphism of a target human, said method comprising the steps :

(A) selecting a known human single nucleotide polymorphism for interrogation;

(B) identifying the sequence of at least one oligonucleotide that flanks said selected single nucleotide polymorphism; said identified sequence being of a length sufficient to permit the identification of primers capable of being used to effect the specific amplification of said flanking oligonucleotide and said polymorphism;

(C) using said primers to effect the amplification of said flanking oligonucleotide and said polymorphism of said single nucleotide polymorphism of said target human; and

(D) interrogating the single nucleotide polymorphism of said amplified polymorphism by genetic bit analysis. --

Please add the following new claims:

-- 32. The method of claim 30, wherein in step (A), said reference organism is a human.

33. The method of claim 31, wherein in step (D), said interrogation is accomplished using a nucleic acid molecule having a nucleotide sequence that specifically hybridizes to an invariant proximal or invariant distal nucleotide sequence of a single nucleotide polymorphism present in DNA of a human, wherein said genetic bit analysis permits specific detection of the single nucleotide polymorphic site (X) of said single nucleotide polymorphism

34. The method of claim 31, wherein said method additionally includes the steps:
(E) comparing said interrogated single nucleotide polymorphism of said target human, with a corresponding single nucleotide polymorphism of a reference human, and determining whether said polymorphisms contain the same single nucleotide at their respective polymorphic sites; and
(F) using said comparison to determine the extent of genetic similarity between said target human and said reference human.

35. The method of claim 34, wherein in step (F), said determination is sufficient to establish that said target human and said reference human are not the same person.

36. The method of claim 34, wherein in step (F), said determination is sufficient to establish that said reference human is not a parent of said target human.

37. The method of claim 34, wherein said reference human has a trait, and said determination of step (F) is sufficient to establish that said target human also has said trait.

38. The method of claim 34, wherein said reference human has a first and second trait, and said determination of step (F) is sufficient to establish a genetic linkage between said traits.

39. The method of claim 34, wherein in step (F), said determination is accomplished by a method having the sub-steps:

(a) incubating a sample of nucleic acid containing said single nucleotide polymorphism of said target human, or said single nucleotide polymorphism of said reference human, in the presence of a nucleic acid primer and at least one dideoxynucleotide derivative, under conditions sufficient to permit a polymerase mediated, template-dependent extension of said primer, said extension causing the incorporation of a single dideoxynucleotide to the 3'-terminus of said primer, said single dideoxynucleotide being complementary to the single nucleotide of the polymorphic site of said polymorphism;

(b) permitting said template-dependent extension of said primer molecule, and said incorporation of said single dideoxynucleotide; and

(c) determining the identity of the nucleotide incorporated into said polymorphic site, said identified nucleotide being complimentary to said nucleotide of said polymorphic site.

40. The method of claim 39, wherein in substep (a), said primer is immobilized to a solid support, and wherein in sub-step (b), said template-dependent extension of said primer is conducted on said immobilized primer.

41. The method of claim 40, wherein in substep (a), said polymerase mediated, template-dependent extension of said primer is conducted in the presence of at least two dideoxynucleotide triphosphate derivatives selected from the group consisting of ddATP, ddTTP, ddCTP and ddGTP, but in the absence of dATP, dTTP, dCTP and dGTP.

42. The method of claim 37, wherein said determination of step (F) comprises the substeps:

(i) determining the identity of a single nucleotide present at a polymorphic site of an equine single nucleotide polymorphism, and being present in more than 51% of a set of reference humans;

(ii) determining whether a single nucleotide present at a polymorphic site of a corresponding single nucleotide polymorphism of said target human has the same identity as the single nucleotide present at said polymorphic site of said 51% of reference humans exhibiting said trait; and

(iii) using said determination of substep (ii) to determine whether said target human will have said particular trait.

43. The method of claim 42, wherein said trait is a genetic disease.

44. The method of claim 42, wherein said trait is a genetic condition.

45. A method for creating a genetic map of unique sequence equine polymorphisms which comprises the steps:

(A) identifying at least one pair of inter-breeding reference humans, wherein each of said pairs of humans is characterized by having a first and a second reference human,

said first reference human having:

two alleles (i) and (ii), said alleles each being single nucleotide polymorphic alleles having a single nucleotide polymorphic site;

said second reference human having:

a corresponding allele (i') to said allele (i) of said first reference human, wherein said allele (i') has a single nucleotide polymorphic site, and wherein the single nucleotide present at said polymorphic site of said allele (i') differs from the single nucleotide present at the polymorphic site of said allele (i) of said first reference human, and